

SEQUENCE LISTING

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FOURNIER, Joëlle  
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GROSJEAN-COURNOYER Marie-Claire

<120> LIPOXYGENASE OVEREXPRESSION IN PLANTS  
AND REDUCTION IN PLANT SENSITIVITY TO  
DISEASES AND TO ATTACKS FROM PATHOGENIC  
ORGANISMS

<130> A36097-PCT-USA-A 072667.0192

<140>  
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<150> PCT/FR02/01943  
<151> 2002-06-06

French Patent Application No. filed June 7, 2001 and French Patent Application No. FR 01/14358 filed November 7, 2001

<150> FR 01/07470  
<151> 2001-06-07

<150> FR 01/14358  
<151> 2001-11-07

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Gly Arg Arg Val Ser Leu Glu Leu Ile Ser Ser Val Asn Ala Asp Pro  
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Ala Asn Gly Leu Gln Gly Lys Arg Ser Lys Ala Ala Tyr Leu Glu Asn  
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Trp Leu Thr Asn Ser Thr Pro Ile Ala Ala Gly Glu Ser Ala Phe Arg  
85 90 95

Val Thr Phe Asp Trp Asp Asp Glu Glu Phe Gly Val Pro Gly Ala Phe  
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Ile Ile Lys Asn Leu His Phe Ser Glu Phe Phe Leu Lys Ser Leu Thr  
115 120 125

Leu Glu Asp Val Pro Asn His Gly Lys Val His Phe Val Cys Asn Ser  
130 135 140

Trp Val Tyr Pro Ala Asn Lys Tyr Lys Ser Asp Arg Ile Phe Phe Ala  
145 150 155 160

Asn Gln Ala Tyr Leu Pro Ser Glu Thr Pro Asp Thr Leu Arg Lys Tyr  
165 170 175

Arg Glu Asn Glu Leu Val Thr Leu Arg Gly Asp Gly Thr Gly Lys Leu  
180 185 190

Glu Glu Trp Asp Arg Val Tyr Asp Tyr Ala Tyr Tyr Asn Asp Leu Gly  
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Asp Pro Asp Lys Gly Gln Asp Leu Ser Arg Pro Val Leu Gly Gly Ser  
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Ser Glu Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Lys Pro Thr  
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Lys Thr Asp Pro Asn Ser Glu Ser Arg Ile Pro Leu Leu Met Ser Leu  
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260 265 270

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275 280 285

Glu Phe Lys Ala Leu Phe Asp Ser Thr His Asn Glu Phe Asp Ser Phe  
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Glu Asp Val Leu Lys Leu Tyr Glu Gly Gly Ile Lys Leu Pro Gln Gly  
305 310 315 320

Pro Leu Leu Lys Ala Ile Thr Asp Ser Ile Pro Leu Glu Ile Leu Lys  
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Gln Val Ile Gln Glu Asp Lys Thr Ala Trp Arg Thr Asp Glu Glu Phe  
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385 390 395 400

Gln Asn Ser Thr Ile Thr Arg Glu Gln Ile Glu Asp Lys Leu Asp Gly  
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His His Asp Ile Leu Met Pro Tyr Leu Arg Arg Ile Asn Thr Ser Thr  
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Asp Thr Lys Thr Tyr Ala Ser Arg Thr Leu Leu Phe Leu Gln Asp Asn  
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565 570 575

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580 585 590

Val Val Tyr Lys Asp Trp Val Phe Pro Glu Gln Ala Leu Pro Thr Asp  
595 600 605

Leu Ile Lys Arg Gly Val Ala Val Glu Asp Ser Ser Ser Pro Leu Gly  
610 615 620

Ile Arg Leu Leu Ile Gln Asp Tyr Pro Tyr Ala Val Asp Gly Leu Lys  
625 630 635 640

Ile Trp Ser Ala Ile Lys Ser Trp Val Thr Glu Tyr Cys Asn Tyr Tyr  
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Tyr Lys Ser Asp Asp Ala Val Gln Lys Asp Thr Glu Leu Gln Ala Trp  
660 665 670

Trp Lys Glu Leu Arg Glu Glu Gly His Gly Asp Lys Lys Asp Glu Pro  
675 680 685

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Ile Thr Ile Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly  
705 710 715 720

Gln Tyr Pro Tyr Ala Gly Tyr Leu Pro Asn Arg Pro Thr Leu Ser Arg  
725 730 735

Asn Phe Met Pro Glu Pro Gly Ser Pro Glu Tyr Glu Glu Leu Lys Thr  
740 745 750

Asn Pro Asp Lys Val Phe Leu Lys Thr Ile Thr Pro Gln Leu Gln Thr  
755 760 765

Leu Leu Gly Ile Ser Leu Ile Glu Ile Leu Ser Arg His Ser Ser Asp  
770 775 780

Thr Leu Tyr Leu Gly Gln Arg Glu Ser Pro Glu Trp Thr Lys Asp Gln  
785 790 795 800

Glu Pro Leu Ser Ala Phe Ala Arg Phe Gly Lys Lys Leu Ser Asp Ile  
805 810 815

Glu Asp Gln Ile Met Gln Met Asn Val Asp Glu Lys Trp Lys Asn Arg  
820 825 830

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Gly Lys Lys Val Lys Gly Thr Val Val Leu Met Lys Lys Asn Val Leu  
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ctt ggt cgg agg gtc tct ctc gag ttg atc agt tct gtt aat gct gat 731  
Leu Gly Arg Arg Val Ser Leu Glu Leu Ile Ser Ser Val Asn Ala Asp  
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cct gca aat ggt tta caa ggg aaa cgc agc aaa gca gca tat ttg gag 779  
Pro Ala Asn Gly Leu Gln Gly Lys Arg Ser Lys Ala Ala Tyr Leu Glu  
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aac tgg cta aca aat agc acc cca ata gca gca ggt gaa tca gca ttt 827  
Asn Trp Leu Thr Asn Ser Thr Pro Ile Ala Ala Gly Glu Ser Ala Phe  
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Arg Val Thr Phe Asp Trp Asp Asp Glu Glu Phe Gly Val Pro Gly Ala  
100 105 110  
ttc att atc aag aac ttg cat ttt agt gag gtc ttc ctc aag tca ctc 923  
Phe Ile Ile Lys Asn Leu His Phe Ser Glu Phe Phe Leu Lys Ser Leu  
115 120 125  
acc ctt gaa gat gtt cct aat cat ggc aaa gtt cat ttt gtc tgt aat 971  
Thr Leu Glu Asp Val Pro Asn His Gly Lys Val His Phe Val Cys Asn  
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tca gac ttc ttg aca ttt gct ttg aaa tcc att gtg cag ttg ctt ctc Ser Asp Phe Leu Thr Phe Ala Leu Lys Ser Ile Val Gln Leu Leu Leu	275                    280                    285	1403
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Phe	Gly	Arg	Glu	Met	Leu	Ala	Gly	Val	Asn	Pro	Val	Ile	Ile	Ser	Arg	
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Leu	Gln	Glu	Phe	Pro	Pro	Lys	Ser	Lys	Leu	Asp	Pro	Lys	Ile	Tyr	Gly	
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Gly	Leu	Thr	Ile	Asp	Glu	Ala	Ile	Lys	Thr	Asn	Arg	Leu	Phe	Ile	Leu	
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Asn	His	His	Asp	Ile	Leu	Met	Pro	Tyr	Leu	Arg	Arg	Ile	Asn	Thr	Ser	
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Thr	Asp	Thr	Lys	Thr	Tyr	Ala	Ser	Arg	Thr	Leu	Leu	Phe	Leu	Gln	Asp	
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Val	Asn	Asp	Ser	Gly	Val	His	Gln	Leu	Ile	Ser	His	Trp	Leu	Asn	Thr	
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His	Ala	Ala	Ile	Glu	Pro	Phe	Val	Ile	Ala	Thr	Asn	Arg	Gln	Leu	Ser	
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Ala	Leu	His	Pro	Ile	Tyr	Lys	Leu	Leu	His	Pro	His	Phe	Arg	Glu	Thr	
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atg	aac	ata	aat	gct	tta	gca	aga	cag	atc	ttg	atc	aac	ggg	ggg	gga	2267
Met	Asn	Ile	Asn	Ala	Leu	Ala	Arg	Gln	Ile	Leu	Ile	Asn	Gly	Gly	Gly	
560							565				570			575		
ctt	ctt	gag	ttg	aca	gtt	ttt	ccg	gcc	aaa	tat	tcc	atg	gaa	atg	tca	2315
Leu	Leu	Glu	Leu	Thr	Val	Phe	Pro	Ala	Lys	Tyr	Ser	Met	Glu	Met	Ser	
580							585				590					
gca	gta	gtt	tac	aaa	gac	tgg	gtt	ttc	cct	gaa	caa	gca	ctt	cct	act	2363
Ala	Val	Val	Tyr	Lys	Asp	Trp	Val	Phe	Pro	Glu	Gln	Ala	Leu	Pro	Thr	

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ggc att cga tta ctg att cag gac tat cca tat gct gtt gat ggg ttg Gly Ile Arg Leu Leu Ile Gln Asp Tyr Pro Tyr Ala Val Asp Gly Leu 625	630	635	2459
aaa att tgg tca gca att aaa agt tgg gta act gaa tac tgc aac tac Lys Ile Trp Ser Ala Ile Lys Ser Trp Val Thr Glu Tyr Cys Asn Tyr 640	645	650	2507
tat tac aaa tca gat gat gcg gtt caa aaa gac act gaa ctc caa gcc Tyr Tyr Lys Ser Asp Asp Ala Val Gln Lys Asp Thr Glu Leu Gln Ala 660	665	670	2555
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cct tgg tgg cct aaa atg cag aca gtg caa gaa ttg ata gac tct tgc Pro Trp Trp Pro Lys Met Gln Thr Val Gln Glu Leu Ile Asp Ser Cys 690	695	700	2651
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cga aat ttc atg cca gag cca gga agt cct gag tat gaa gag ctc aag Arg Asn Phe Met Pro Glu Pro Gly Ser Pro Glu Tyr Glu Glu Leu Lys 740	745	750	2795
aca aat ccg gat aag gta ttc ctc aaa aca atc act cct cag ctg cag Thr Asn Pro Asp Lys Val Phe Leu Lys Thr Ile Thr Pro Gln Leu Gln 755	760	765	2843
aca ctg ctt ggc att tcc ctc ata gag atc ttg tca agg cat tct tcg Thr Leu Leu Gly Ile Ser Leu Ile Glu Ile Leu Ser Arg His Ser Ser 770	775	780	2891
gat aca ctt tac ctc ggg caa agg gaa tca cct gaa tgg aca aag gat Asp Thr Leu Tyr Leu Gly Gln Arg Glu Ser Pro Glu Trp Thr Lys Asp 785	790	795	2939
caa gaa cca ctt tca gct ttt gcg agg ttt gga aag aag ctg agt gat Gln Glu Pro Leu Ser Ala Phe Ala Arg Phe Gly Lys Lys Leu Ser Asp 800	805	810	2987
atc gag gat cag att atg cag atg aat gtc gat gag aaa tgg aag aac Ile Glu Asp Gln Ile Met Gln Met Asn Val Asp Glu Lys Trp Lys Asn 820	825	830	3035

agg tcg ggt cct gtt aaa gtt cca tac acc ttg ctc ttc ccc aca agt 3083  
Arg Ser Gly Pro Val Lys Val Pro Tyr Thr Leu Leu Phe Pro Thr Ser  
835 840 845

gaa gga gga ctt act ggc aaa gga att cct aac agt gtg tca ata tag 3131  
Glu Gly Gly Leu Thr Gly Lys Gly Ile Pro Asn Ser Val Ser Ile  
850 855 860

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